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Sequence Listing could not be accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=9; day=23; hr=13; min=47; sec=2; ms=955;]

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Reviewer Comments:

<210> 3

<211> 1647

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<223> GroEL-Asp490Cys DNA sequence

<220>

<221> mutation

<222> (1468)..(1470)

<223> GAC to TCG

<400> 3

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gataaatctt tcggtgccacc gaccatcacc aaagatggtg	240
tttccgttgc tcgtgaaatc gaactggaaag acaagttcga	300
aaacatgggt ggcgcagatgg tgaaagaagt tgccctctaa	360
gccaacgacg ctgcaggcga cggtaccacc actgcaaccg	420
tactggctca ggctatcatc actgaaggta tgaaagctgt	480
tgctgcgggc atgaacccga tggacctgaa acgtggtata	540
gacaaagctg ttaccgctgc agttgaagaa ctgaaagcgc	600
tgtccgtacc gtgctctgac tctaaagcga ttgctcaggt	660
tggtactatc tccgctaact ccgacgaaac cgtaggtaaa	720
ctgatcgctg aagcgatgga caaagtcggt aaagaaggcg	780
ttatcaccgt tgaagacggc accggctctgc aggacgaact	840
ggacgtggtt gaaggtatgc agttcgaccg tggctacctg	900
tctccttact tcatcaacaa gcccggaaact ggcgcagtag	
aactggaaag cccgttcatc ctgctggctg acaagaaaat	
ctccaaacatc cgccaaatgc tgccggttct ggaagccgtt	
gccaaaggcag gcaaaccgct gctgatcatc gctgaagatg	
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gcgtggcatc gtgaaagttg ctgcagttaa agctccgggc	
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atctctgaag agatcggtat ggagctggaa aaagcaaccc tggaaagacct gggtcaggct	960
aaacgcgttg tgatcaacaa agacaccacc accatcatcg atggcgtggg cgaagaagct	1020
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gaaccgtctg ttgttgctaa caccgttaaa ggccggcgacg gcaactacgg ttacaacgca	1440
gcaaccgaag aatacggcaa catgatctgc atgggtatcc tggaccacaa caaagtaacc	1500

The above <223> response describing the base mutation at location 1468-1470 is incorrect: the mutation is "tgc" not "tcg".

Application No: 10583179 Version No: 1.0

Input Set:

Output Set:

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Finished: 2008-08-25 16:14:50.245
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 375 ms
Total Warnings: 0
Total Errors: 0
No. of SeqIDs Defined: 8
Actual SeqID Count: 8

SEQUENCE LISTING

<110> Agency for Science, Technology and Research

<120> Protein Separation Device

<130> 51571-4

<140> 10583179

<141> 2008-08-25

<150> US 60/530,608

<151> 2003-12-19

<160> 8

<170> PatentIn version 3.3

<210> 1

<211> 1647

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<223> GroEL wildtype DNA sequence

<400> 1

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gataaatctt tcgggcacc gaccatcacc aaagatgg	tttccgttgc tcgtgaaatc	180
gaaactggaa	gacatgggt	240
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cggttctgtc	tgcggtgttgc tggatcgatccat gatatcgaa ccctgactgg cggtaccgt	1620
gttaccgacc	tgccgaaaaaa cgatcgacat gacttaggcgt gatcgatccat gatatcgaa ccctgactgg cggtaccgt	

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1647

<210> 2
<211> 548

<212> PRT
<213> Escherichia coli

<220>
<221> misc_feature
<223> GroEL wildtype amino acid sequence

<400> 2
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Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
20 25 30

Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65 70 75 80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Ala Thr Val Leu Ala
85 90 95

Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
100 105 110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val
115 120 125

Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
130 135 140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
145 150 155 160

Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
165 170 175

Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
180 185 190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
195 200 205

Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
210 215 220

Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val

225 230 235 240
Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
245 250 255
Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys
260 265 270

Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
275 280 285
Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
290 295 300
Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala
305 310 315 320
Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val
325 330 335
Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln
340 345 350
Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg
355 360 365
Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
370 375 380
Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu
385 390 395 400
His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
405 410 415
Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln
420 425 430
Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu
435 440 445
Ala Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val
450 455 460
Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala
465 470 475 480
Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro
485 490 495
Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly
500 505 510
Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp
515 520 525

<220>
<221> misc_feature
<223> GroEL Asp490Cys amino acid sequence

<220>
<221> SITE
<222> (490)..(490)
<223> D to C

<400> 4

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Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
20 25 30

Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65 70 75 80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Ala Thr Val Leu Ala
85 90 95

Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
100 105 110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val
115 120 125

Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
130 135 140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
145 150 155 160

Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
165 170 175

Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
180 185 190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
195 200 205

Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
210 215 220

Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val
225 230 235 240

Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
245 250 255

Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys
260 265 270

Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
275 280 285

Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
290 295 300

Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala
305 310 315 320

Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val
325 330 335

Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln
340 345 350

Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg
355 360 365

Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
370 375 380

Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu
385 390 395 400

His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
405 410 415

Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln
420 425 430

Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu
435 440 445

Ala Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val
450 455 460

Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala
465 470 475 480

Ala Thr Glu Glu Tyr Gly Asn Met Ile Cys Met Gly Ile Leu Asp Pro
485 490 495

Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly
500 505 510

Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp
515 520 525

Ala Ala Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met
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Gly Gly Met Met
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<210> 5
<211> 1647
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<223> GroEL apical domain RYD modification DNA sequence

<220>
<221> mutation
<222> (598)..(606)
<223> CTGTCTCCT to CGTTATGAT

<220>
<221> mutation
<222> (1468)..(1470)
<223> GAC to TGC

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gataaatctt tcgggtcacc gaccatcacc aaagatggta tttccgttgc tcgtgaaatc
gaactggaag acaagttcga aaatatgggt ggcgcagatgg tgaaagaagt tgccctctaaa
gcaaacgacg ctgcaggcga cggtaccacc actgcaaccg tactggctca ggctatcatc
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gcaaccgttgc aatacggcaaa catgatctgc atgggtatcc tggatccaa caaagtaact
cggttgc tgcgttgc gtcgttgc agtgcgttgc gtcgttgc tgcgttgc gtcgttgc
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<210> 6
<211> 548
<212> PRT
<213> Escherichia coli

<220>
<221> misc_feature
<223> GroEL apical domain RYD modification

<220>
<221> SITE
<222> (200)..(202)
<223> LSP to RYD

<220>
<221> site
<222> (490)..(490)
<223> D to C

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Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
20 25 30

Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
35 40 45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
50 55 60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
65 70 75 80

Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala T